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RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/10/088,830   TIME: 13:06:06

Input Set : **A:\BTGI0025.ST25.txt**
Output Set: **N:\CRF3\04092002\J088830.raw**

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   3 <110> APPLICANT: Gutierrez-Armenta, Crisanto
   4         Ramirez-Parra, Elena
   6 <120> TITLE OF INVENTION: Wheat DP Proteins And Uses Thereof
   8 <130> FILE REFERENCE: BTGI-0025
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/088,830
C--> 10 <141> CURRENT FILING DATE: 2002-03-22
  10 <150> PRIOR APPLICATION NUMBER: P9902127
  11 <151> PRIOR FILING DATE: 1999-09-24
  13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09325
  14 <151> PRIOR FILING DATE: 2000-09-25
  16 <150> PRIOR APPLICATION NUMBER: P9902474
  17 <151> PRIOR FILING DATE: 1999-11-11
  19 <160> NUMBER OF SEQ ID NOS: 16
  21 <170> SOFTWARE: PatentIn version 3.1
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  24 <211> LENGTH: 1089
  25 <212> TYPE: DNA
  26 <213> ORGANISM: Triticum monococcum
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  30 <222> LOCATION: (20)..(802)
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  43 agt gtc ccc ccg ctt ccc gaa gcg ggc ggt aat gcg gtc caa agg aag     148
  44 Ser Val Pro Pro Leu Pro Glu Ala Gly Gly Asn Ala Val Gln Arg Lys
  45             30                  35                  40
  47 ggg gct gtt gac ccg gat aaa gat agg aag aag gag aag gct gcg gca     196
  48 Gly Ala Val Asp Pro Asp Lys Asp Arg Lys Lys Glu Lys Ala Ala Ala
  49     45                  50                  55
  51 ccg agg atc acc ggt tgg ggg ctc cgc gag tac agc aaa ata gtt tgt     244
  52 Pro Arg Ile Thr Gly Trp Gly Leu Arg Glu Tyr Ser Lys Ile Val Cys
  53 60                  65                  70                  75
  55 gag aaa gtt gaa gcc aaa gga aga aca aca tac aat gag gtt gca gac     292
  56 Glu Lys Val Glu Ala Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp
  57             80                  85                  90
  59 gaa att tat tca gag ctg aag tcc atg gca cat att ggt caa ggg ttt     340
  60 Glu Ile Tyr Ser Glu Leu Lys Ser Met Ala His Ile Gly Gln Gly Phe
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64 Asp Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp Ala Phe Asn Val Leu
65          110                 115                 120
67 att gca ctt cgt gtt att gca aaa gaa aaa aag gag ata cgg tgg atg    436
68 Ile Ala Leu Arg Val Ile Ala Lys Glu Lys Lys Glu Ile Arg Trp Met
69          125                 130                 135
71 ggc ctt tca aat tac aga tat gaa aaa ata aag aag ctt gag gaa gtt    484
72 Gly Leu Ser Asn Tyr Arg Tyr Glu Lys Ile Lys Lys Leu Glu Glu Val
73 140                 145                 150                 155
75 cgt aaa gaa ctc gtc aac aag att agg aac aag aag gca ctc ctc cag    532
76 Arg Lys Glu Leu Val Asn Lys Ile Arg Asn Lys Lys Ala Leu Leu Gln
77                  160                 165                 170
79 gaa atc gaa aaa cag ttt gat gat ctc caa aac atc aag tta cgt aac    580
80 Glu Ile Glu Lys Gln Phe Asp Asp Leu Gln Asn Ile Lys Leu Arg Asn
81          175                 180                 185
83 caa aca ctg gaa agc tca gca gag aat gtt aat ggc atc cgc ctt cca    628
84 Gln Thr Leu Glu Ser Ser Ala Glu Asn Val Asn Gly Ile Arg Leu Pro
85          190                 195                 200
87 ttc gta ttg gtc aag aca tct agg aaa gca agg gtg gaa att gag att    676
88 Phe Val Leu Val Lys Thr Ser Arg Lys Ala Arg Val Glu Ile Glu Ile
89          205                 210                 215
91 tca gat gac tcg aag ttt gcc cat ttc gag ttc aat ggt gca cca ttc    724
92 Ser Asp Asp Ser Lys Phe Ala His Phe Glu Phe Asn Gly Ala Pro Phe
93 220                 225                 230                 235
95 aca ttg cat gat gat ctc tca atc ctt gag ggg gta agg cgt aac agc    772
96 Thr Leu His Asp Asp Leu Ser Ile Leu Glu Gly Val Arg Arg Asn Ser
97                  240                 245                 250
99 ata gga aga gct ggc cgc gcc acc ctt cac tagagactca agaatattac    822
100 Ile Gly Arg Ala Gly Arg Ala Thr Leu His
101              255                 260
103 aaatgaatta aaagtgttag aactggcaca gccggattct tttgcacagc tatgtatagc    882
105 tatatatcct catgaaaact tgacctagtt tataggacag tctctcaggc ttgagaagat    942
107 tttaacctgc aaattttgtc tccttttgt gcctagcagg ttattaggtc tcagatagat   1002
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129 Pro Glu Ala Gly Gly Asn Ala Val Gln Arg Lys Gly Ala Val Asp Pro
130          35                  40                  45
133 Asp Lys Asp Arg Lys Lys Glu Lys Ala Ala Ala Pro Arg Ile Thr Gly
134     50                  55                  60
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137 Trp Gly Leu Arg Glu Tyr Ser Lys Ile Val Cys Glu Lys Val Glu Ala
138 65                  70                  75                  80
141 Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp Glu Ile Tyr Ser Glu
142                     85                  90                  95
145 Leu Lys Ser Met Ala His Ile Gly Gln Gly Phe Asp Glu Lys Asn Ile
146                     100                 105                 110
149 Arg Arg Arg Val Tyr Asp Ala Phe Asn Val Leu Ile Ala Leu Arg Val
150             115                 120                 125
153 Ile Ala Lys Glu Lys Lys Glu Ile Arg Trp Met Gly Leu Ser Asn Tyr
154         130                 135                 140
157 Arg Tyr Glu Lys Ile Lys Lys Leu Glu Glu Val Arg Lys Glu Leu Val
158 145                 150                 155                 160
161 Asn Lys Ile Arg Asn Lys Lys Ala Leu Leu Gln Glu Ile Glu Lys Gln
162                 165                 170                 175
165 Phe Asp Asp Leu Gln Asn Ile Lys Leu Arg Asn Gln Thr Leu Glu Ser
166             180                 185                 190
169 Ser Ala Glu Asn Val Asn Gly Ile Arg Leu Pro Phe Val Leu Val Lys
170         195                 200                 205
173 Thr Ser Arg Lys Ala Arg Val Glu Ile Glu Ile Ser Asp Asp Ser Lys
174     210                 215                 220
177 Phe Ala His Phe Glu Phe Asn Gly Ala Pro Phe Thr Leu His Asp Asp
178 225                 230                 235                 240
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185 Arg Ala Thr Leu His
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190 <211> LENGTH: 1974
191 <212> TYPE: DNA
192 <213> ORGANISM: Triticum monococcum
194 <220> FEATURE:
195 <221> NAME/KEY: CDS
196 <222> LOCATION: (166)..(1539)
197 <223> OTHER INFORMATION:
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203 tccggcgagc cccccccgat gccctcctgc cttctctgaa gccgaagacg cccatcgctc       120
205 ccgggagtcg ggggtcccgc agcgcgcgat cgcgagatcg ggctt atg tct ggg ggc       177
206                                                    Met Ser Gly Gly
207                                                     1
209 ggc agg ccg ccg gct gcg caa aaa atc ctg cag tct ctg cgc ccg ccc       225
210 Gly Arg Pro Pro Ala Ala Gln Lys Ile Leu Gln Ser Leu Arg Pro Pro
211 5                   10                  15                  20
213 ccg gtg ttc tcc acg ccg tcg cgg cct ccc ttc gcc tca ccc gac gac       273
214 Pro Val Phe Ser Thr Pro Ser Arg Pro Pro Phe Ala Ser Pro Asp Asp
215                     25                  30                  35
217 tac cac cgc ttt cat gcg ccg act acc cct tct gcc act ggc tcc ggc       321
218 Tyr His Arg Phe His Ala Pro Thr Thr Pro Ser Ala Thr Gly Ser Gly
219                     40                  45                  50
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222 Gly Ile Gly Ser Gly Gly Val Gly Gly Asp Ile Asp Glu Gly Leu Val
223          55                  60                  65
225 atc cgg acg cag cta aaa aga aaa gcc aca cgc gaa gaa aat aat gcg     417
226 Ile Arg Thr Gln Leu Lys Arg Lys Ala Thr Arg Glu Glu Asn Asn Ala
227     70                  75                  80
229 gct gag tcg agt gac tgt atg att gtc acc act gga gtt act ggc aat     465
230 Ala Glu Ser Ser Asp Cys Met Ile Val Thr Thr Gly Val Thr Gly Asn
231 85                  90                  95                 100
233 ccg cta ctc acc cca gtg tct gga aaa gct gtt aag aat tct aaa tca     513
234 Pro Leu Leu Thr Pro Val Ser Gly Lys Ala Val Lys Asn Ser Lys Ser
235             105                 110                 115
237 aag act aag aac aat aaa gct ggg cct cag aca cct acg cca aat gtt     561
238 Lys Thr Lys Asn Asn Lys Ala Gly Pro Gln Thr Pro Thr Pro Asn Val
239             120                 125                 130
241 ggc tca cca ctc aat cca tca act cct gct ggt act tgc cgc tat gac     609
242 Gly Ser Pro Leu Asn Pro Ser Thr Pro Ala Gly Thr Cys Arg Tyr Asp
243             135                 140                 145
245 agt tcg tta gga ctt ctg aca aag aag ttc atc aat ttg ctg aag caa     657
246 Ser Ser Leu Gly Leu Leu Thr Lys Lys Phe Ile Asn Leu Leu Lys Gln
247         150                 155                 160
249 gct gag gat ggc att cta gat ttg aat aat gct gca gaa aca cta gag     705
250 Ala Glu Asp Gly Ile Leu Asp Leu Asn Asn Ala Ala Glu Thr Leu Glu
251 165                 170                 175                 180
253 gtt caa aag cga cgc ata tat gac atc aca aat gtc ctc gaa gga att     753
254 Val Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile
255             185                 190                 195
257 ggt ctt ata gaa aag aca ctt aaa aac aga att cgt tgg aag ggc ttg     801
258 Gly Leu Ile Glu Lys Thr Leu Lys Asn Arg Ile Arg Trp Lys Gly Leu
259         200                 205                 210
261 gat gat tca gga gtg gaa tta gat aat ggc ctt tca ggt ttg cag aca     849
262 Asp Asp Ser Gly Val Glu Leu Asp Asn Gly Leu Ser Gly Leu Gln Thr
263             215                 220                 225
265 gaa gtt gaa aat ctt aat ttg cag gag caa gcc tta gat gag cgt ata     897
266 Glu Val Glu Asn Leu Asn Leu Gln Glu Gln Ala Leu Asp Glu Arg Ile
267     230                 235                 240
269 agt gat atg cgc gaa aag cta agg ggg tta acg gaa gat gag aac agt     945
270 Ser Asp Met Arg Glu Lys Leu Arg Gly Leu Thr Glu Asp Glu Asn Ser
271 245                 250                 255                 260
273 caa aga tgg ctc tat gtg acg gaa gat gat atc aag gga tta ccc tgc     993
274 Gln Arg Trp Leu Tyr Val Thr Glu Asp Asp Ile Lys Gly Leu Pro Cys
275             265                 270                 275
277 ttt cag aat gaa act cta att gca ata aaa gct cct cat ggt act aca    1041
278 Phe Gln Asn Glu Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr
279             280                 285                 290
281 ctt gaa gta cct gat cct gat gag gct ggt gat tat ctc cag agg aga    1089
282 Leu Glu Val Pro Asp Pro Asp Glu Ala Gly Asp Tyr Leu Gln Arg Arg
283         295                 300                 305
285 tac aga atc gta tta aga agt acc ctg ggt cca ata gat gtt tac tta    1137
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Input Set : A:\BTGI0025.ST25.txt
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286 Tyr Arg Ile Val Leu Arg Ser Thr Leu Gly Pro Ile Asp Val Tyr Leu
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289 gtt agt caa ttt gac gat gga ttt gag aat ttg ggt ggt gct gcg aca    1185
290 Val Ser Gln Phe Asp Asp Gly Phe Glu Asn Leu Gly Gly Ala Ala Thr
291 325                 330                 335                 340
293 cct cca agg cat aca aat gtc cca aaa cct gga cct tgt gaa gac tta    1233
294 Pro Pro Arg His Thr Asn Val Pro Lys Pro Gly Pro Cys Glu Asp Leu
295             345             350                 355
297 cat gca aca aac gct aca caa agc agc aaa tca atc aat gtg gaa tat    1281
298 His Ala Thr Asn Ala Thr Gln Ser Ser Lys Ser Ile Asn Val Glu Tyr
299             360             365                 370
301 aat att cag cac agg cag aat act cca caa gat cct agt tct tca aat    1329
302 Asn Ile Gln His Arg Gln Asn Thr Pro Gln Asp Pro Ser Ser Ser Asn
303         375             380                 385
305 gat tat gga ggg atg aca agg ata atc cct tca gat gtt aat act gat    1377
306 Asp Tyr Gly Gly Met Thr Arg Ile Ile Pro Ser Asp Val Asn Thr Asp
307         390             395                 400
309 gct gat tac tgg ctc cta aca gag ggt gat gtt agt att act gac atg    1425
310 Ala Asp Tyr Trp Leu Leu Thr Glu Gly Asp Val Ser Ile Thr Asp Met
311 405                 410                 415                 420
313 tgg gaa aca gca cca gaa gtg cag tgg gac acc gct gtg ttt tta cct    1473
314 Trp Glu Thr Ala Pro Glu Val Gln Trp Asp Thr Ala Val Phe Leu Pro
315                 425             430                 435
317 gaa gat gtt agc atc cca cat gca cat cat agt ccg cgg atg cag gtt    1521
318 Glu Asp Val Ser Ile Pro His Ala His His Ser Pro Arg Met Gln Val
319             440             445                 450
321 cca agc atg gat caa cca taaggtcatg gcggtgaaaa cttgacatat          1569
322 Pro Ser Met Asp Gln Pro
323         455
325 ggaattcctg gagtgctgtt tcagaaaata ctgatttcaa aatggaaaga tcagggcagc  1629
327 aagttcagac tgatcaccgt tctgaatttg ctgtttgtta tggagacgat tggtgccaac  1689
329 taacttatca gtctgctgcc ttgtttgttc tggcacctgt ccttcagttg aaaaggcgcc  1749
331 catgtgcata ttgcaccttg aattcgggct gctatgcaca ttcggtatct gctttatttc  1809
333 tctaactgag tatattttgc aaggcaatag tggctctgta gctctcttgg gaattaatac  1869
335 gaatcttttt gagcaaaaac agtagggaag tcccctgttg tgactctttc attatataaa  1929
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355 Ser Pro Asp Asp Tyr His Arg Phe His Ala Pro Thr Thr Pro Ser Ala
356             35              40                  45
359 Thr Gly Ser Gly Gly Ile Gly Ser Gly Gly Val Gly Gly Asp Ile Asp
360         50              55                  60
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VERIFICATION SUMMARY   DATE: 04/09/2002
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date